What is claimed is:

1. A method for detecting a fusion nucleic acid comprising the steps of:

a) providing a sample containing a first single-stranded fusion nucleic acid comprising a splice junction;

b) contacting under nucleic acid amplification conditions:

the first single-stranded fusion nucleic acid,

a first primer capable of hybridizing to the fusion nucleic acid at a first primer binding site located 3' to the splice junction site, and

at least one nucleic acid polymerase activity;

c) amplifying the fusion nucleic acid in a nucleic acid amplification reaction using the first primer to produce a plurality of second nucleic acid strands complementary to at least a portion of the first single-stranded fusion nucleic acid that contains the splice junction site, wherein each second nucleic acid strand comprises:

a complementary splice junction site,

a first probe binding site located 3' to and not overlapping the complementary splice junction site, and

a second probe binding site located 5' to and not overlapping the complementary splice junction site, wherein the second probe binding site overlaps or is located 3' to sequence complementary to the first primer binding site;

d) hybridizing the second nucleic acid strands with an oligonucleotide probe under hybridization conditions that permit hybridization of the probe to the first or the second probe binding site, thereby forming a probe:target hybrid; and

e) detecting the probe:target hybrid as an indication of the presence of the fusion nucleic acid in the sample.

2. The method of Claim 1, wherein the first single-stranded fusion nucleic acid is an mRNA, the first primer is a promoter-primer, the polymerase activity comprises an RNA polymerase activity, and the oligonucleotide probe is of the same sense as the mRNA and is capable of binding to the first probe binding site.

3. The method of Claim 1, wherein the first single-stranded fusion nucleic acid is a mRNA, wherein the second nucleic acid strands are complementary RNA, and further comprising contacting the second nucleic acid strand with a second primer or promoter-primer capable of hybridizing to a second primer binding site located 3' to both the complementary splice junction and the first probe binding site, and wherein the amplifying step uses an RNA polymerase activitiy, a DNA-directed DNA polymerase activity and an RNA-directed DNA polymerase activity.

4. The method of Claim 1, wherein the oligonucleotide probe is capable of binding to the second probe binding site and incapable of forming a stable hybridization complex with the first single-stranded fusion nucleic acid.

5. The method of Claim 1, wherein the fusion nucleic acid is a *bcr-abl* fusion mRNA and wherein the oligonucleotide probe is capable of binding to a *bcr*-derived nucleotide base sequence in the second nucleic acid strands.

6. The method of Claim 1, wherein step a) further comprises preparing the sample containing the fusion nucleic acid by:

contacting a biological sample comprising the fusion nucleic acid with a solution comprising:

a buffer,

about 150 mM to about 1 M of a soluble salt,

about 0.5% to about 1.5% (v/v) of a non-ionic detergent, and

a solid support to which is joined an immobilized oligonucleotide comprising a nucleotide base sequence capable of forming, directly or indirectly, a stable hybridization complex with an RNA under conditions permitting the formation of the stable hybridization complex; and

separating the hybridization complex joined to the solid support from unhybridized sample components.

7. The method of Claim 6, wherein the fusion nucleic acid is mRNA.

8 The method of Claim 7, wherein the nucleotide base sequence of the immobilized oligonucleotide comprises a poly-T sequence.

9. A method of detecting a fusion mRNA transcript produced as a result of a chromosomal translocation, comprising:

a) providing a sample containing a fusion mRNA transcript comprising a splice junction;

b) contacting under nucleic acid amplification conditions:

the fusion mRNA transcript,

a first primer capable of hybridizing to the fusion mRNA transcript at a first primer binding site derived from a first chromosomal region and located 3' to the splice junction site, and

at least one enzyme having nucleic acid polymerase activity;

c) amplifying the fusion mRNA transcript in a nucleic acid amplification reaction that uses the first primer to produce a plurality of second nucleic acid strands complementary to at least a portion of the fusion mRNA transcript containing the splice junction site, wherein each second nucleic acid strand comprises:

a complementary splice junction site,

a first probe binding site located 3' to and not overlapping the complementary splice junction site, wherein the first probe binding site is derived from a second chromosomal region, and

a second probe binding site located 5' to and not overlapping the complementary splice junction site, wherein the second probe binding site is derived from a third chromosomal region and overlaps or is located 3' to sequence complementary to the first primer binding site;

d) hybridizing the second nucleic acid strands with an oligonucleotide probe capable of hybridizing to the second nucleic acid strands at the first or the second probe binding site but incapable of hybridizing to the fusion transcript, thereby forming a hybridization complex of the probe and the second nucleic acid strand; and

e) detecting the hybridization complex as an indication of the presence of the fusion transcript in the sample.

10. The method of Claim 9, wherein the amplifying step uses only a first primer that is a promoter primer and the enzyme has an RNA polymerase activity, and wherein the hybridizing step uses an oligonucleotide probe capable of hybridizing to the second nucleic acid at the first probe binding site.

11. The method of Claim 9, wherein the first probe binding site and the second probe binding site are derived from different locations on the same chromosome in a eukaryotic cell, and the fusion mRNA transcript detected results from an intrachromosomal translocation.

12. The method of Claim 9, wherein the first probe binding site is derived from a different chromosome than the chromosome from which the second probe binding site is derived, and the fusion mRNA transcript detected results from a translocation involving different chromosomes.

13. The method of Claim 12, wherein the fusion mRNA transcript results from a translocation of human chromosomes selected from the group consisting of: t(1;19), t(2;5), t(2;13), t(4;11), t(6;9), t(8;21), t(9;11), t(9;22), t(11;14), t(11;19), t(11;22), t(12;21), t(14;18) and t(15;17) translocations.

14. The method of Claim 13, wherein the fusion mRNA transcript results from a human t(9;22) translocation and the oligonucleotide probe comprises a *bcr*-derived sequence or an *abl*-derived sequence.

15. One or more oligonucleotides suitable for use in the method of Claim 14, have a sequence selected from the group consisting of SEQ ID NO:1 to SEQ ID NO:23, SEQ ID NO:26 and SEQ ID NO:27.

16. The method of Claim 9, wherein the amplifying step uses an RNA polymerase activity, a DNA-directed DNA polymerase activity, and an RNA-directed DNA polymerase activity, and further uses a second primer or promoter primer capable of hybridizing under amplification conditions to a nucleotide sequence of a complementary RNA produced during the amplifying step.

17. The method of Claim 16, wherein the RNA-directed DNA polymerase activity and DNA-directed DNA polymerase activity are supplied by a reverse transcriptase.

18. The method of Claim 9, further comprising the steps of amplifying an internal control transcript in the sample by using the first primer and then hybridizing a second oligonucleotide probe capable of hybridizing to the complement of the internal control transcript but incapable of hybridizing to the complement of the fusion mRNA transcript thereby forming in internal control hybridization complex, and detecting the presence of the internal control hybridization complex in the sample, thereby providing an internal standard.

19. A method of preparing a sample containing RNA suitable for amplification, comprising the steps of:

a) providing a biological sample comprising unpurified RNA;

b) mixing the biological sample with a solution comprising:

a buffer at a pH of about 6.5 to about 8.5,

at least about 150 mM of a soluble salt,

an effective amount of a non-ionic detergent sufficient to release RNA from the biological sample without causing viscosity due to release of chromosomal DNA, and

a solid support to which is joined an immobilized oligonucleotide comprising a nucleotide base sequence capable of forming a stable immobilized oligonucleotide:RNA hybridization complex;

c) separating the hybridization complex joined to the solid support from unhybridized sample components; and

d) then washing the hybridization complex joined to the solid support with a solution having sufficient salt concentration to maintain the hybridization complex.

20. The method of Claim 19, wherein the biological sample is uncoagulated blood, plasma or bone marrow.